MARKED-UP AMENDED CLAIMS 6-15, 18, 20 and 22

6. (Amended) Method according to [one of claims] claim 3 [to 5], further characterized in that the oligonucleotide or PNA sequences bound to the surface contain 5-bromouracil structural units.

7. (Amended) Method according to [at least one of the preceding claims] claim 1, further characterized in that the immobilized complementary oligonucleotide sequences contain modified bases, ribose or backbone units.

8. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that the genomic DNA sample is propagated in b) in the form of several amplified fragments, so that at least 0.01% of the total genome is amplified.

9. (Amended) Method according to [at least one of the preceding claims] claim 1, further characterized in that the mixture of amplified DNA fragments is bound to a surface, on which a multiple number of different points is arranged, each of which can bind different portions of the amplified DNA sample.

10. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that a set of probes is used in d), which contains the dinucleotide sequence 5'-CpG-3' only once in each probe and the probes otherwise contain either no cytosine or no guanine bases.

11. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that a bisulfite or pyrosulfite or disulfite solution or a mixture of the indicated solutions is used together with other reagents for the specific or sufficiently selective conversion of cytosine to uracil.

12. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that the surface used for the immobilization of amplified sample DNA is also the sample holder for a mass spectrometer.

13. (Amended) Method according to [at least one of claims 1 to 11] claim 1 , further characterized in that the surface used for the immobilization of amplified sample DNA is introduced as a whole, prior to f), onto a sample holder for a mass spectrometer.

14. (Amended) Method according to [one of claims 1 to 13] claim 1, further characterized in that the hybridized probes are stripped from the immobilized amplified DNA samples before, after or by contact with a matrix.

15. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that the probes are nucleic acids, which bear one or more mass tags.

18. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that the probes are modified nucleic acid molecules.

20. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that the probes are prepared by combinatory synthesis.

22. (Amended) Method according to [one of the preceding claims] claim 1, further characterized in that the probes are prepared as sublibraries and these are provided with different mass and/or charge tags.